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Figure 1A

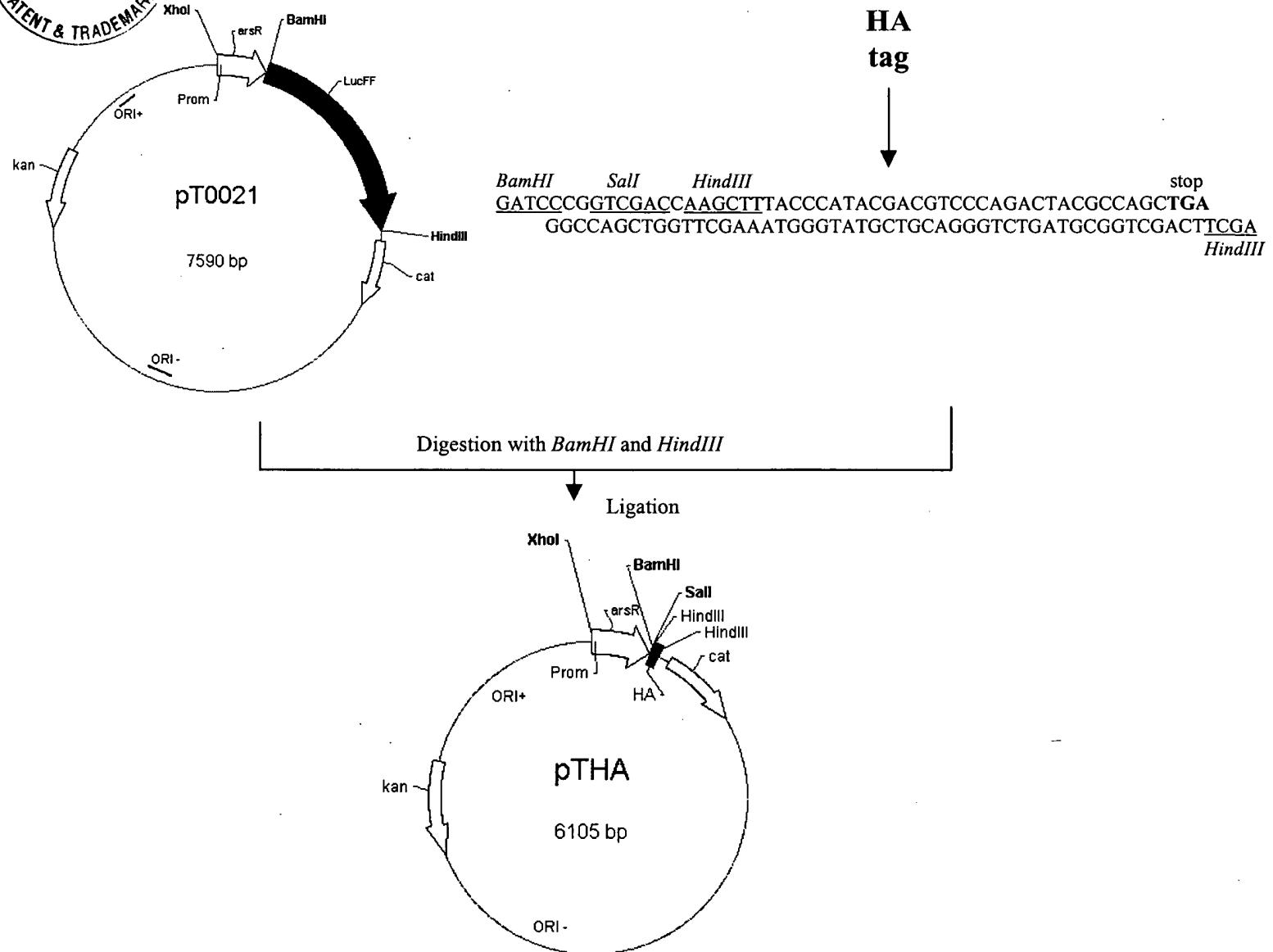
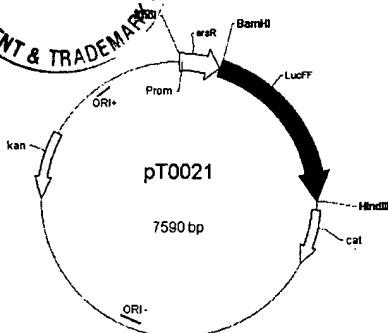




Figure 1B

PCR of pT0021 with XhoF and BamHNR

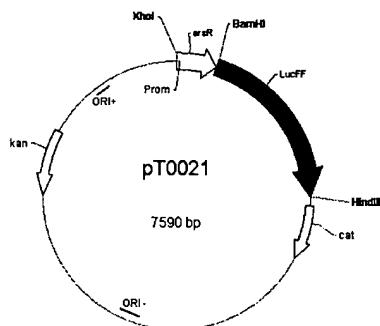


XhoF-5'-AATTCTCGAGTAATAACAT-3
XhoI

AAATCAGGTGACTGTTGAGAAAGGAGGCGGATCCG-BamHNR
Stop of arsR RBS *BamHI*

Digestion with *XhoI* and *BamHI*

Ligation



Modified between stop of arsR to *BamHI*

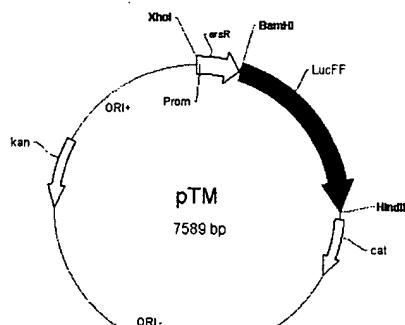
PCR of pT0021 with LucFFB and LucFFH

LucFFB-5'-CGGGATCCATGAGGGGTTCCGAAGACG
BamHI Start of LucFF Original *BamHI* was modified

GAAAGTCCAATTGTTAAGCTTGGG-LucFFH
Stop of *HindIII* LucFF

Digestion with *BamHI* and *HindIII*

Ligation

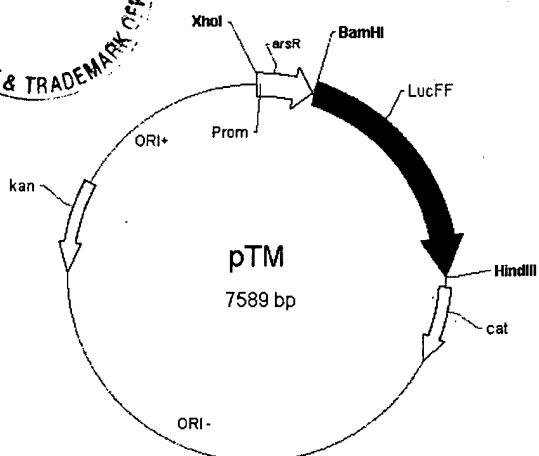


- Modified in the vicinity of *BamHI*
- Cloning site for ORFs: *BamHI* and *HindIII*
- No additional codons in the induced protein

Prom arsR LucFF
XhoI CTCGAG-ATG-----TGAGAAAAGGAGGCGGATCCATG-----TAAGCTT
RBS *BamHI* *HindIII*



Figure 1C



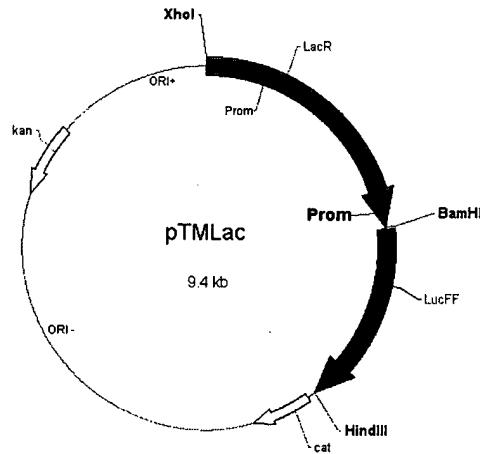
PCR of *Staphylococcus aureus* DNA with lacF and LacR

LacF-5'-CCGCTCGAGCTCCAAATTCCAAAACAG
XhoI

GTAAAAAAGGAGTCTTATTGGATCCCG-LacR
BamHI

Digestion with *Xho*I and *Bam*HI

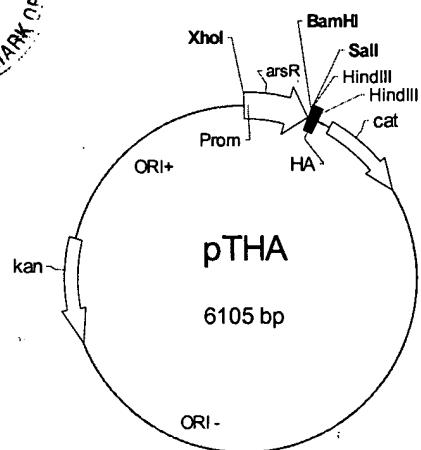
Ligation



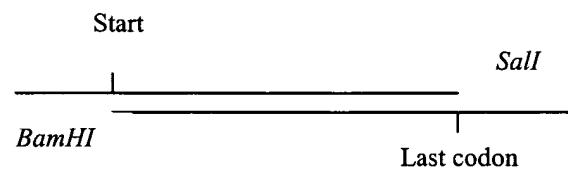
The diagram illustrates the *lacZ* promoter region. It features two inverted TATA boxes (Prom) at the top, with arrows pointing to the right. Below these are the *LacR* and *LacA* binding sites, each consisting of a sequence (TTG and CTA respectively) followed by a dashed line. The sequence continues with a long stretch of DNA: CTCGAG (with a *Xba*I site below it), TTG (with a *Bam*HI site below it), CTA, and AGGAGTCTTATTGGATCCATG.



Figure 2A



PCR of phage DNA with
ORF specific primers



Digestion with *BamHI* and *Sall*

Ligation

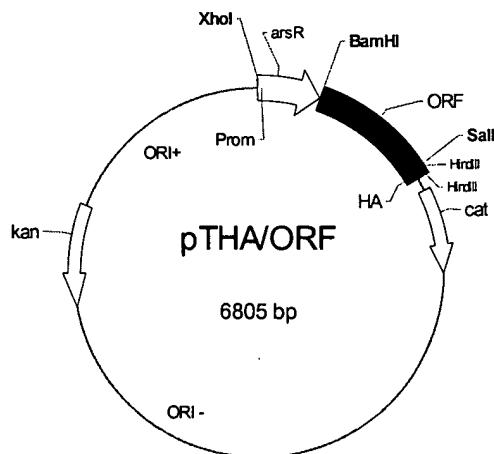
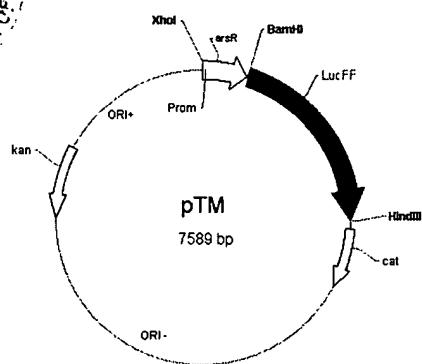
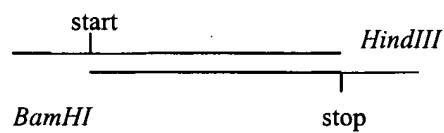




Figure 2B



PCR of phage DNA with
ORF specific primers



Digestion with *BamHI* and *HindIII*

Ligation

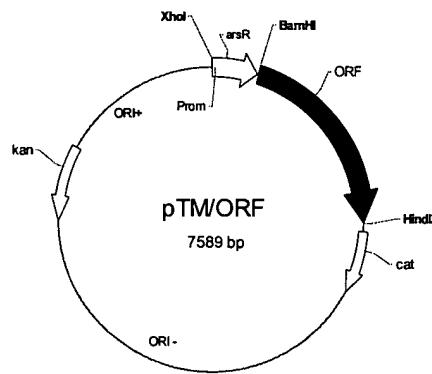
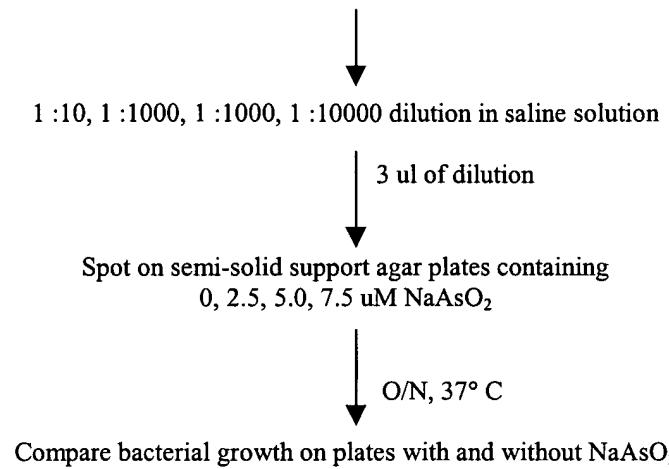




Figure 3

3A: Functional assay on semi-solid support medium

O/N culture inoculated from frozen stock
of phage ORF *Staphylococcus aureus* RN4220 transformants



3B: Functional assay in liquid medium

O/N culture inoculated from frozen stock
of phage ORF *Staphylococcus aureus* RN4220 transformants

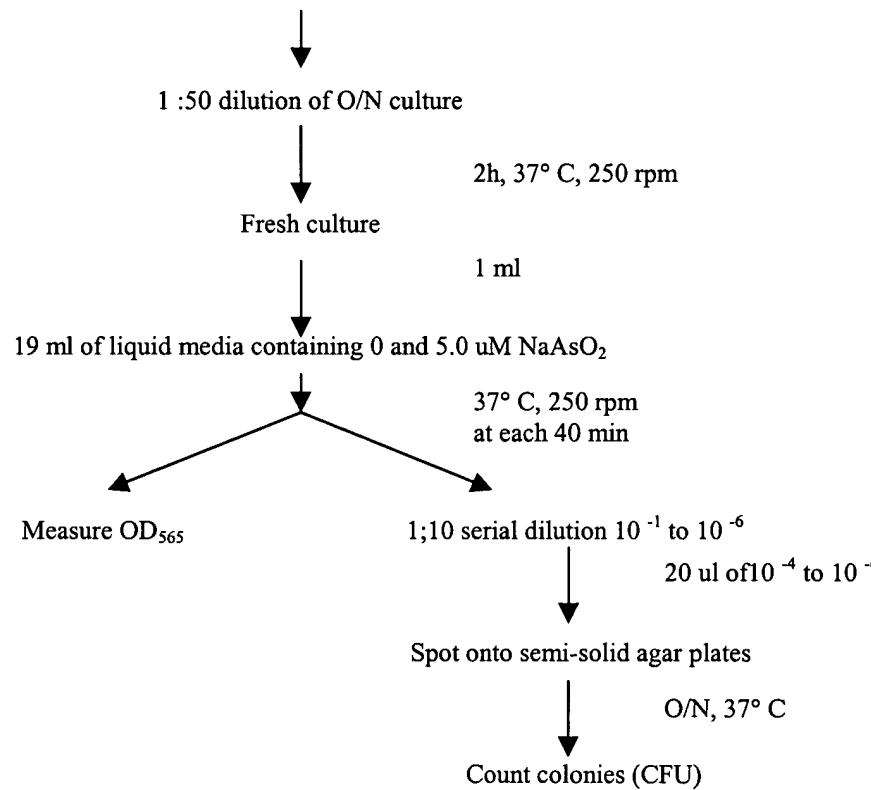




Figure 4A

44AHJD ORFs tested for functional analysis

UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796



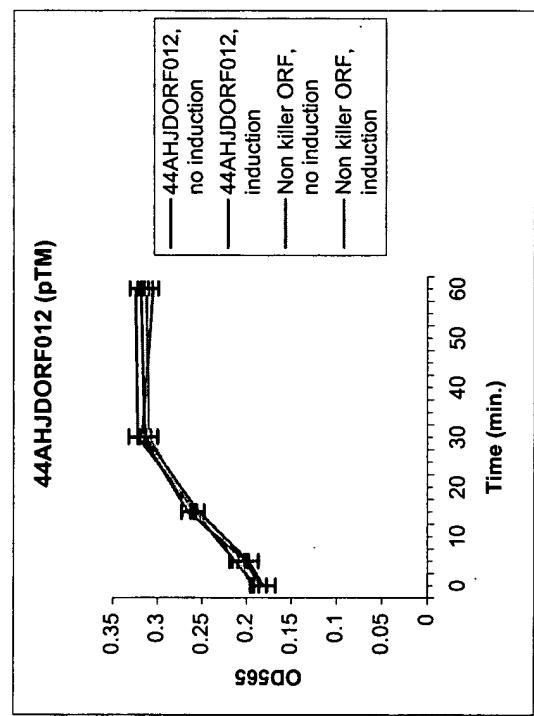
Figure 4B

		Semi-solid support media			
ORF ID	<i>Staphylococcus aureus</i> transformants	Without induction		With induction (5 μ M sodium arsenite)	
44AHJDORF12	Clone1				
	Clone2				
	Clone3				
44AHJDORF25	Clone1				
	Clone2				
	Clone3				
Control 77ORF30	Clone1				



Figure 5A

Frame 1



Frame 2

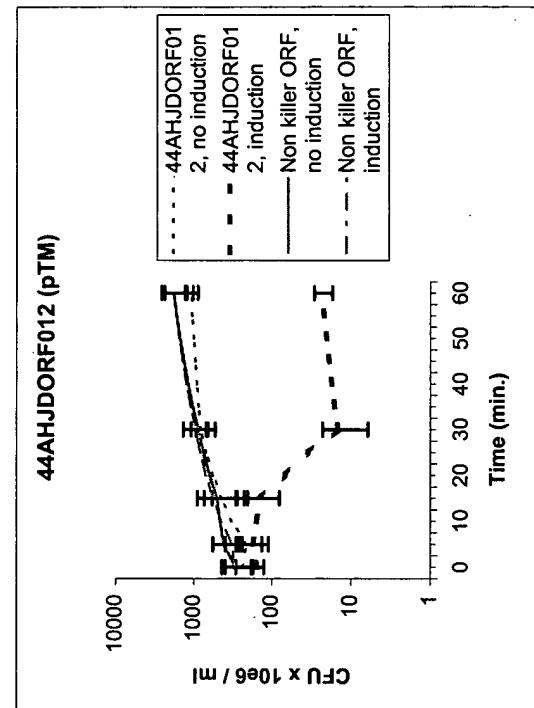
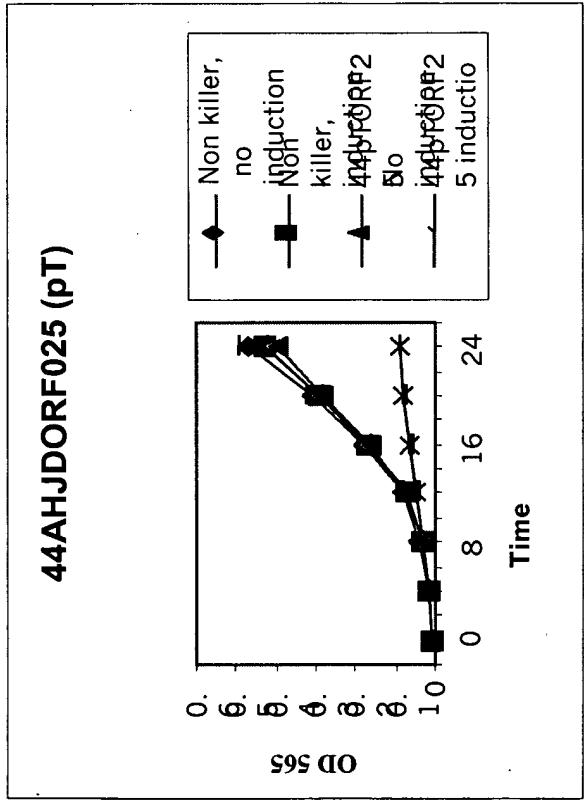
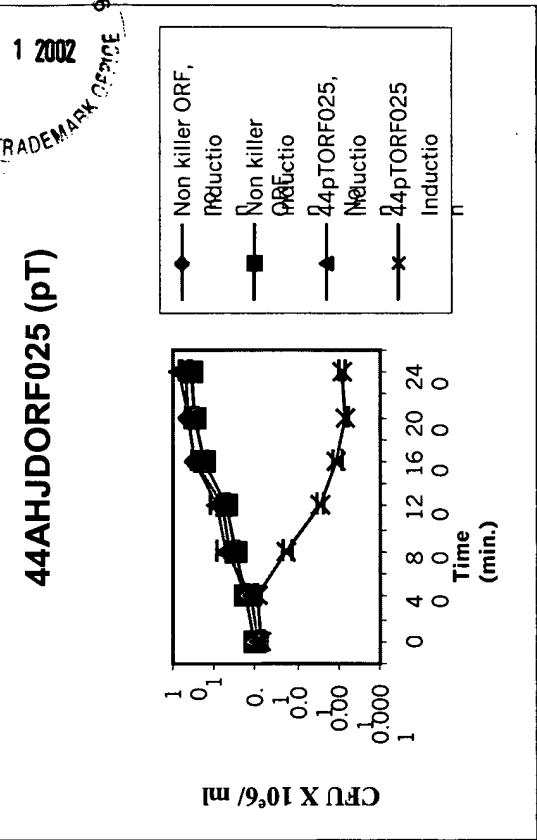


Figure 5B

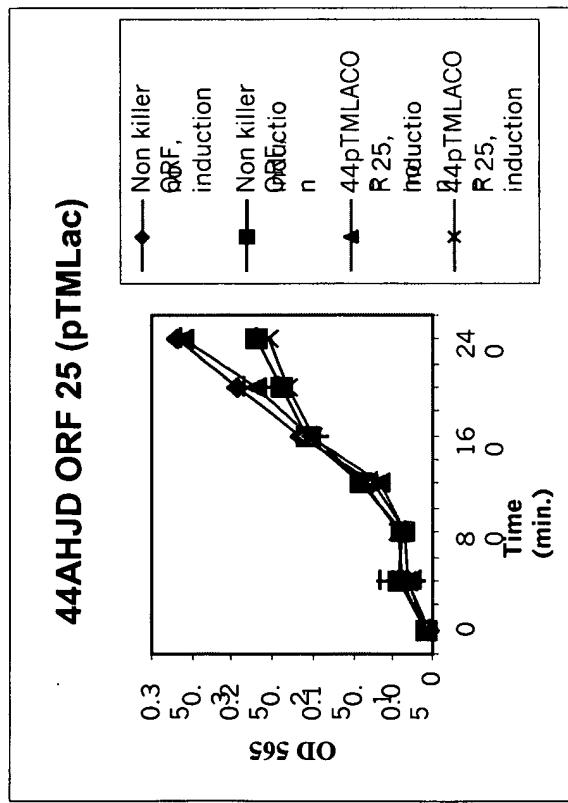
Frame 1



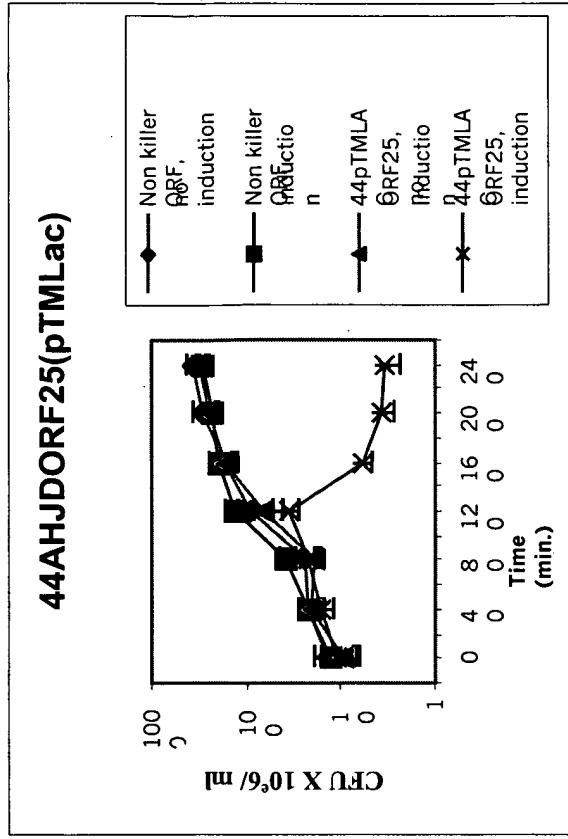
Frame 2



Frame 3



Frame 4



44AHJDORF025 (pT)

44AHJDORF25(pTMLac)



FIGURE 6

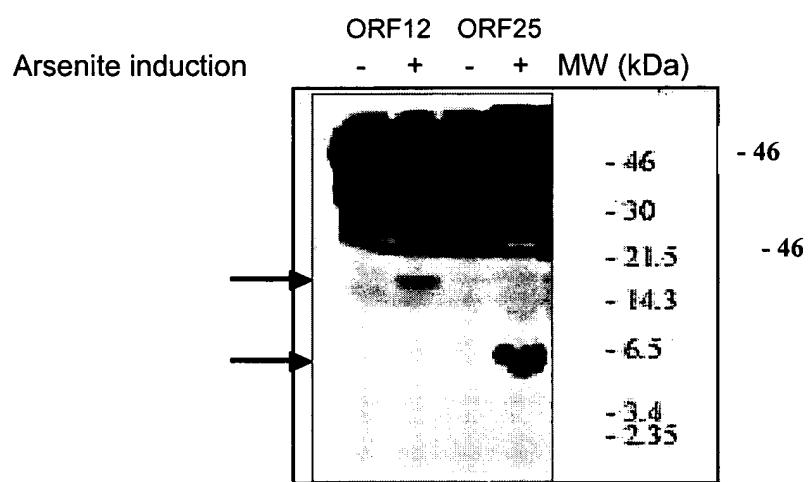
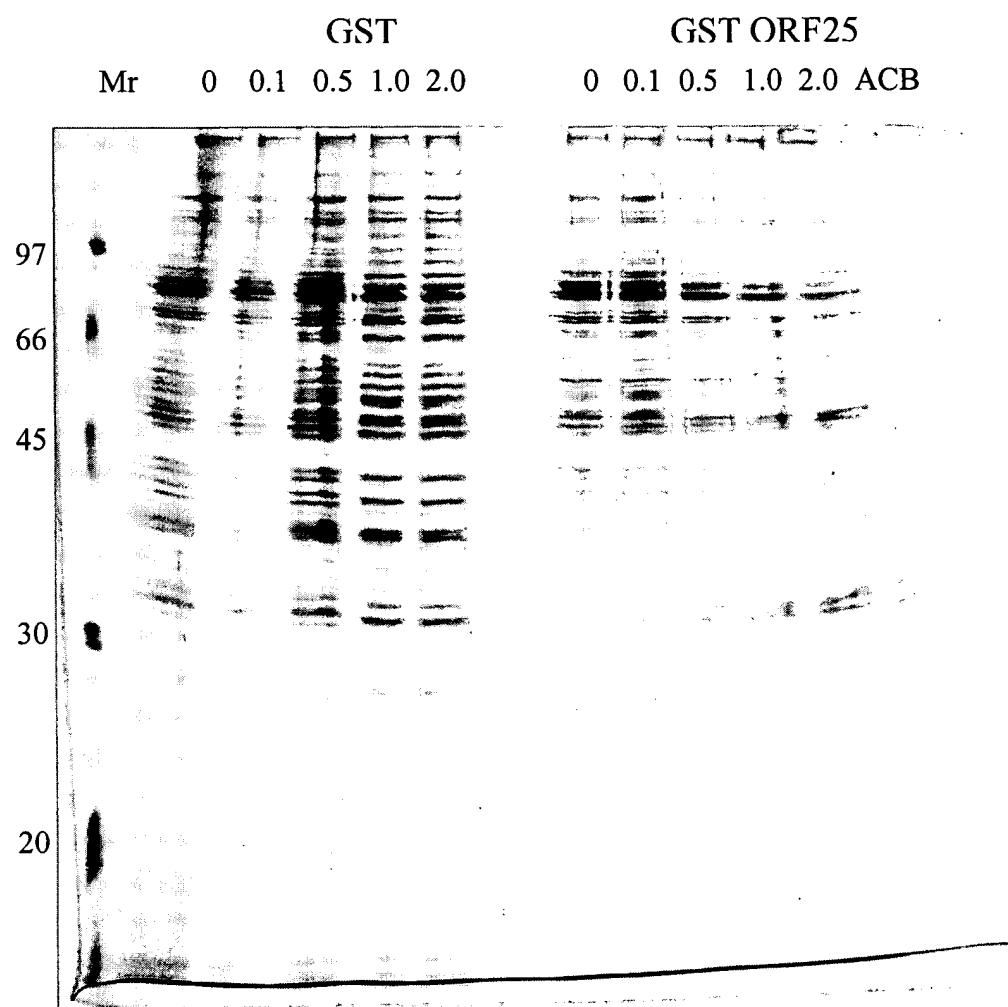




FIGURE 7A





<div[](Figure7B.jpg)

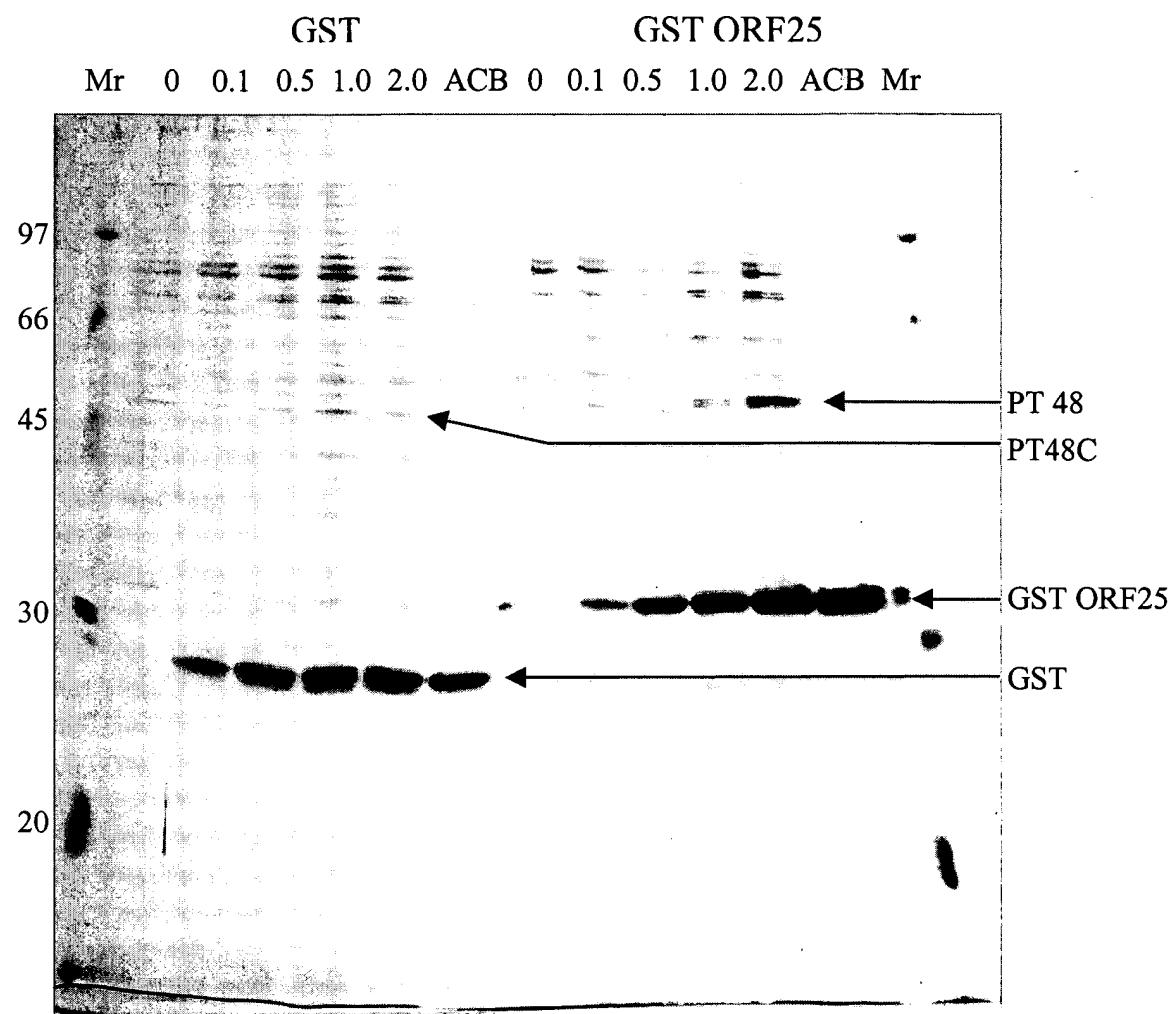




FIGURE 8

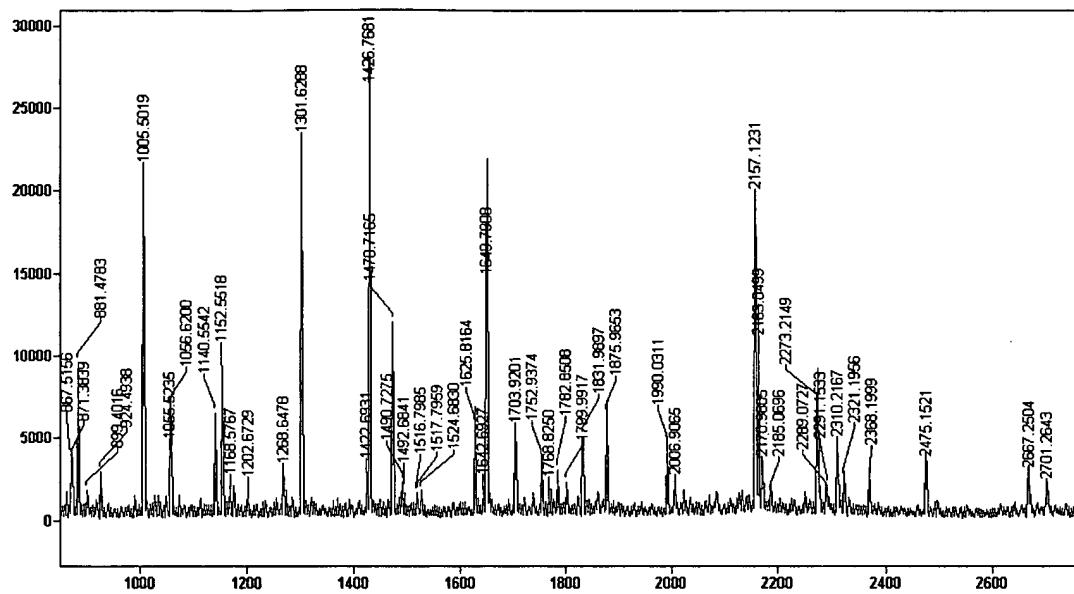




FIGURE 9

Details for : PT48

gi|1706496|sp|P50029|DP3B STAAU DNA POLYMERASE III, BETA CHAIN

gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - *Staphylococcus aureus*

Sample ID : PT 48

Number of Measured Peptides : 40

Number of Matched Peptides : 17

Coverage of protein sequence : 68%

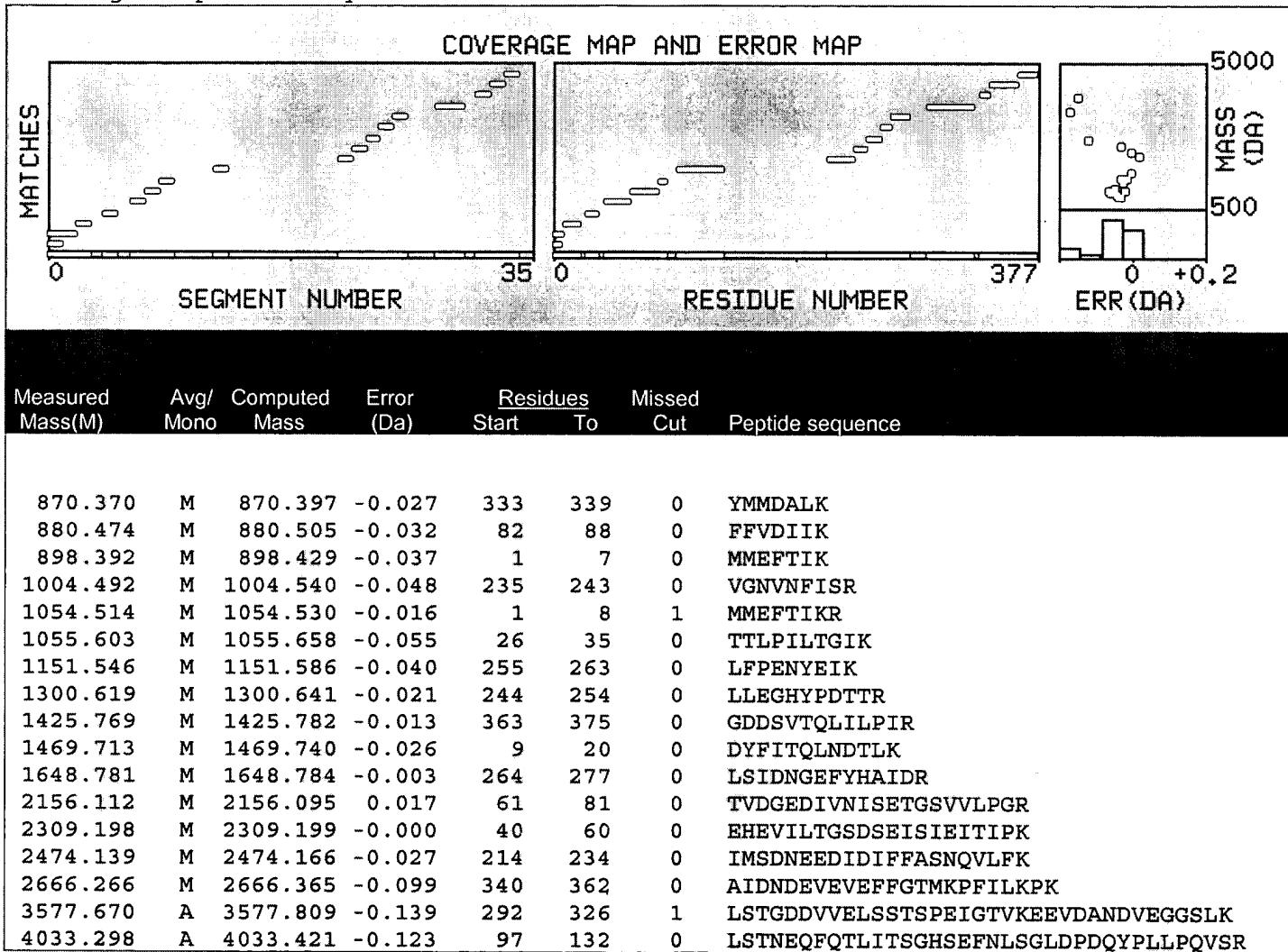




FIGURE 10

Figure 10A : SEQ ID NO : 166

ATGATGGAATTCACTATTAAAAGAGATTATTTATTACACAATTAAATGACACATTAAAA
GCTATTCAACCAAGAACAAACATTACCTATTTAACTGGTATCAAAATCGATGCGAAAGAA
CATGAAGTTATTAACGGTTCAGACTCTGAAATTCAATAGAAATCACTATTCCCTAAA
ACTGTAGATGGCGAAGATATTGTCATATTCAAGAACACAGGCTCAGTAGTACTCCTGGA
CGATTCTTGTGATATTAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT
GAACAATTCCAGACATTAATTACATCAGGTATTCTGAATTAAATTAAAGTGGCTTAGAT
CCAGATCAATATCCATTACCTCAAGTTCTAGAGATGACGCAATTCAATTGTCGGTA
AAAGTGCCTAAAAACGTGATTGACAAACAAATTTCAGTGTCCACCTCAGAAACACGC
CCAGTACTAAGTGGTGTGAACGGCTTACAAAGAAAATGAATTAAATATGCACAGCGACT
GACTCACACCCTGGCTGTAAGAAAGTTGAGTAGAAGATGTTCTGAAAACAAAAAT
GTCATCATTCCAGGTAAAGGCTTAGCTGAATTAAATAAAATTATGTCGACAATGAAGAA
GACATTGATATCTCTTGCTCAAACCAAGTTTATTAAAGTGGAAATGTGAACCTT
ATTCTCGATTATTAGAAGGACATTACCTGATACAACACGTTATTCCCTGAAAACAT
GAAATTAAATTAGTATAAGACAATGGGGAGTTTATCATGCGATTGATCGTGCCTTTA
TTAGCGCGTGAAGGTGGTAAACGTTATTAAATTAGTACAGGTGATGACGTTGAA
TTGTCTCTACATCACCAGAAATTGGTACTGAAAAGAAGAAGTTGATGCAAACGATGTT
GAAGGTGGTAGCCTGAAAATTCACTCTAAATATGATGGATGTTAAAAGCA
ATCGATAATGATGAGGTTGAAGTTGAATTCTCGGTACAATGAAACCATTATTCTAAAA
CCAAAAGGTGACGACTCGGTAAACGCAATTAAATTACCAATCAGAACTTACTAA

Figure 10B : SEQ ID NO : 167

>gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -
Staphylococcus aureus

MMEFTIKRDYFITQLNDTLKAISPRTTLPILTGIKIDAKEHEVILTGSDSEISIEITIPKTVGDGDIVNI
SETGSVVLPGRRFFVDI IKKLPKGDKVKLSTNEQFQTLITSGHSEFNLSGLDPDQYPLPQVSRDDAIQLSV
KVLKNVIAQTNFAVSTSETRPVLTGVNWLIQENELICTADSHRLAVRKLQLEDVSENKNVII PGKALAE
LNKIMSDNEEDIDIFFASNQVLFKVGNNFISRLLEGHYPDTTRLFPENYEIKLSIDNGEFYHAIDRASL
LAREGGNNVIKLSTGDDVVELSSTSPEIGTVKEEV DANDVEGGSLKISFNSKYMMDALKAIIDNDEVEVEF
FGTMKPFILKPKGDDSVTQLILPIRTY